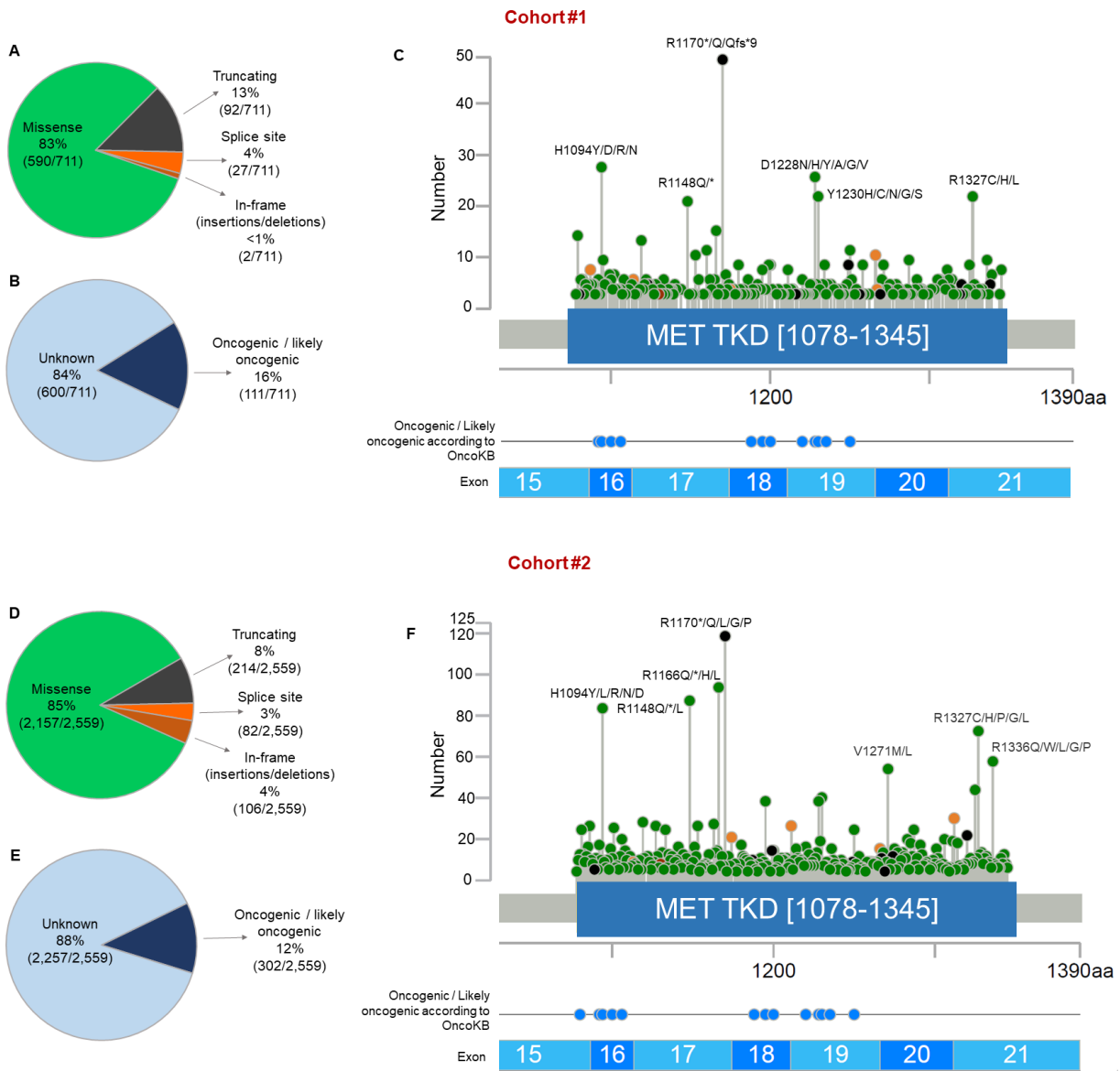


## Supplementary Figure 2



**Supplementary Figure 2. Overview of *MET* TKD mutations detected in pan-cancer cohorts.** (A) Type (missense, truncating, splice site, in-frame) of *MET* TKD mutations detected in the cohort #1 (711 *MET* TKD mutations among 664 unique patients with a tumor harboring *MET* TKD mutations without concurrent *MET*ex14 alterations). (B) Type of *MET* TKD mutations according to OncoKB annotation (biological function: oncogenic / likely oncogenic, unknown) detected in cohort #1. (C) Distribution of *MET* TKD mutations across *MET* kinase domain for cohort #1. (D) Type (missense, truncating, splice site, in-frame) of *MET* TKD mutations detected in cohort #2 (2,559 *MET* TKD

mutations among 2,477 unique patients with a tumor harboring *MET* TKD mutations without concurrent *MET*ex14 alterations). (E) Type of *MET* TKD mutations according to OncoKB annotation (biological function: oncogenic / likely oncogenic, unknown) detected in cohort #2. (F) Distribution of *MET* TKD mutation across MET kinase domain for cohort #2.